

1/24

2/24	3/24
4/24	5/24
6/24	7/24

Fig. 1

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-60 tgaaaagatagaataaatggcctcgtg

1 ATGGCGCGGCCAGCGCTGCTGGGCGAG

1 M A R P A L L G E

61 GGCCAAGTTGCCGCGGCCACAGAAGTT

21 G Q V A A A T E V

121 GAAAATCTCTGCACGATAATATGGACG

41 E N L C T I I W T

181 ACTCTCAGATATTTTAGTCACTTTGAT

61 T L R Y F S H F D

241 CATCGTAAAGAGGAATTACCCCTGGAT

81 H R K E E L P L D

301 AGTGCCAATGAAAGTGAGAAGCCTAGC

101 S A N E S E K P S

361 GGTGATCCTGAGTCCGCTGTGACTGAG

121 G D P E S A V T E

421 AAGTGTTCTGCTCCCTGGAAGGAAT

141 K C S W L P G R N

Fig. 1(i)

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ccgaattcggcacgagccgagggcgagggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG

L L V L L L W T A T V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT

E K I C L Q V G S Q C

CCTTTGGTGAAAAAGTGCATCTCACCCCCTGAA

P L V K K C I S P P E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG

L K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

T S P D T H Y T L Y Y

Fig. 1(ii)

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481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTTCCTTTAAATTGACTAAA
181	I A C S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L W S D W S E

Fig. 1(iii)

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CAATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
V E P S F E H Q N V Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
I R P S C K I V S L T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
I K H L L L K N G A L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
F R S R C L T Y E V E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
N I L E V E E D K C Q

GGTACAAGTTGTTTCCAACCTCCCTGGTGTCTT
G T S C F Q L P G V L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
R V K T N K L C F D D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC
A Q S I G K E Q N S T

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Fig. 1(iv)

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1021 TTCTACACCACCATGTTACTCACCATT
 341 F Y T T M L L T I

1081 CTTTTTACCTGAAAAGGCTTAAGATC
 361 L F Y L K R L K I

1141 ATTTTAAAGAAATGTTTGGAGACCAG
 381 I F K E M F G D Q

1201 ATCTATGAGAAACAATCCAAAGAAGAA
 401 I Y E K Q S K E E

1261 AAAGCAGCTCCTTGAtgggggagaagtg
 421 K A A P *

1321 gatttattgcattctccatttggtatc
 1381 cttgaaaaacaggcagctcctaagagc
 1441 ccaaacccaaaggagctccttccaaga
 1501 ccctaaaagcagatgttttgccaaatc
 1561 accatcaattcatctaatacaggaattg

Fig. 1(v)

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CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
P V F V A V A V I I L

ATTATATTTCTCCAATTCCTGATCCTGGCAAG
I I F P P I P D P G K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
N D D T L H W K K Y D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
T D S V V L I E N L K

atttcttttcttgccttcaatgtgaccctgtgaa

tgggggacttggttaaataagaaactgaaactact
cacaggtcttgatgtgacttttgcattgaaaac
aaagcaagagttcttctcgttccttgttccaat
cccaaactagaggacaaagacaaggggacaatg
tgatggcttcctaaggaatctctgcttgctctg

Fig. 1(vi)

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NR4 EXPRESSION IN MOUSE TISSUES

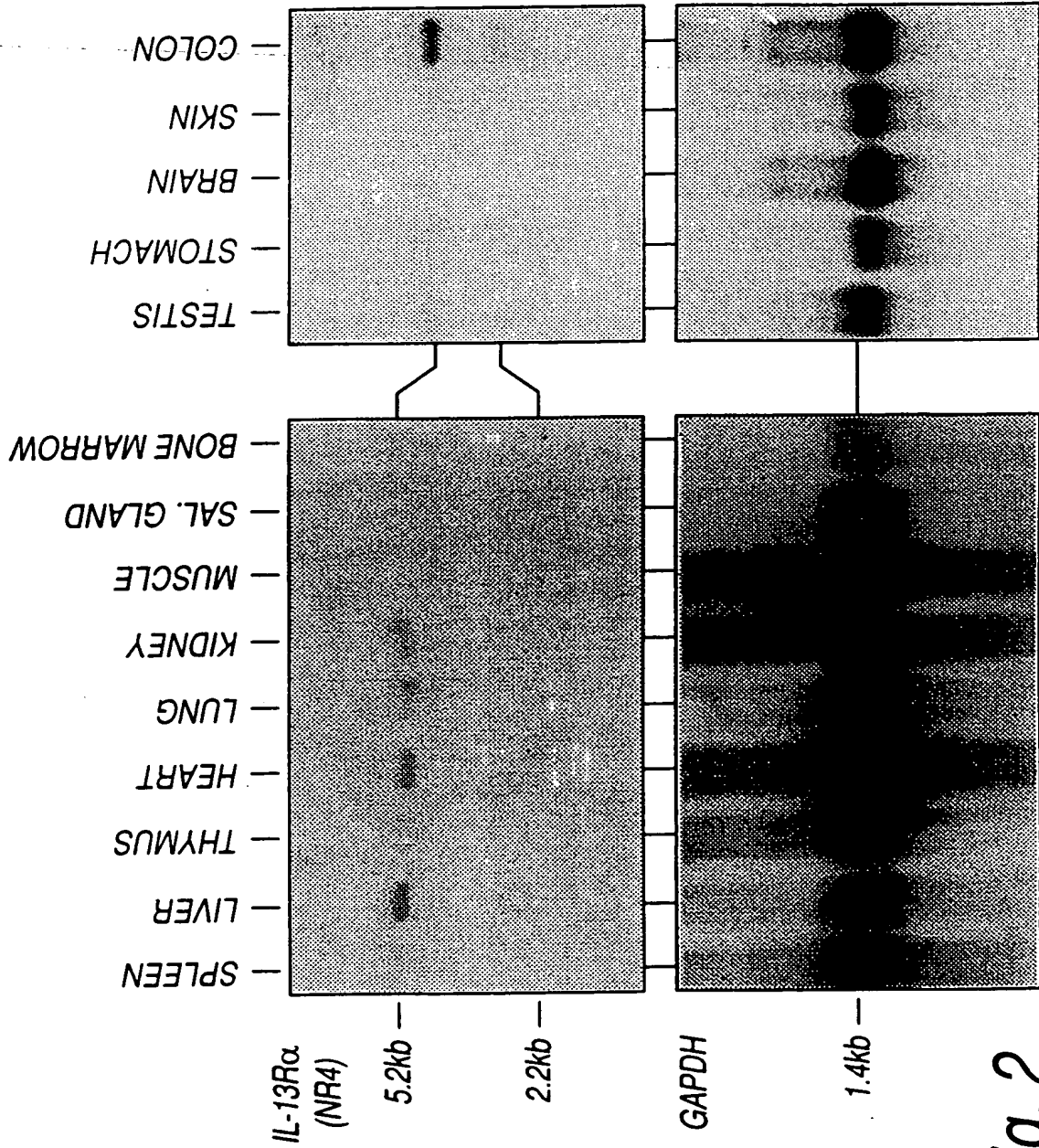


Fig. 2

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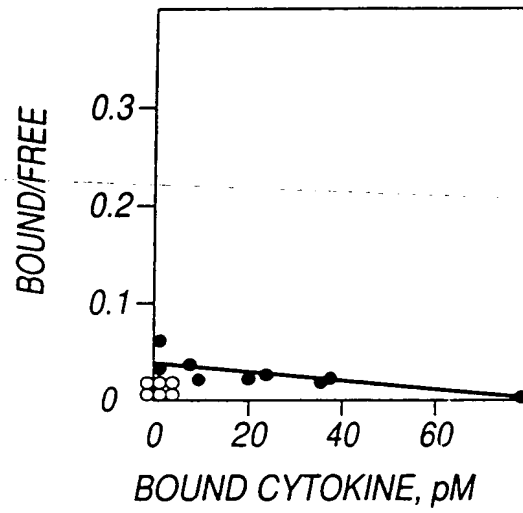


Fig. 3(A)

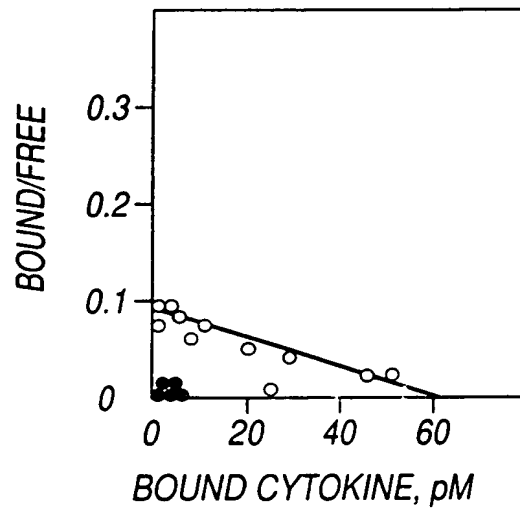


Fig. 3(B)

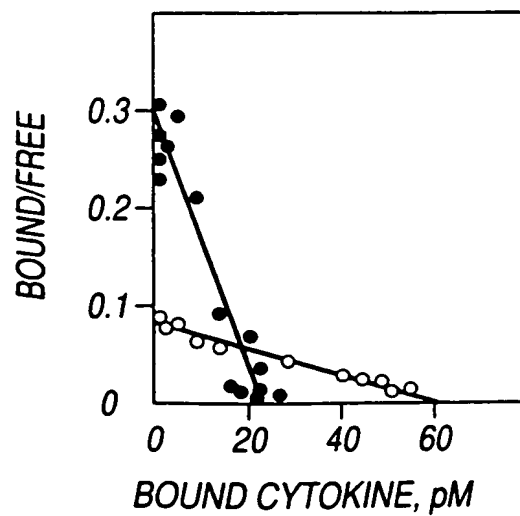
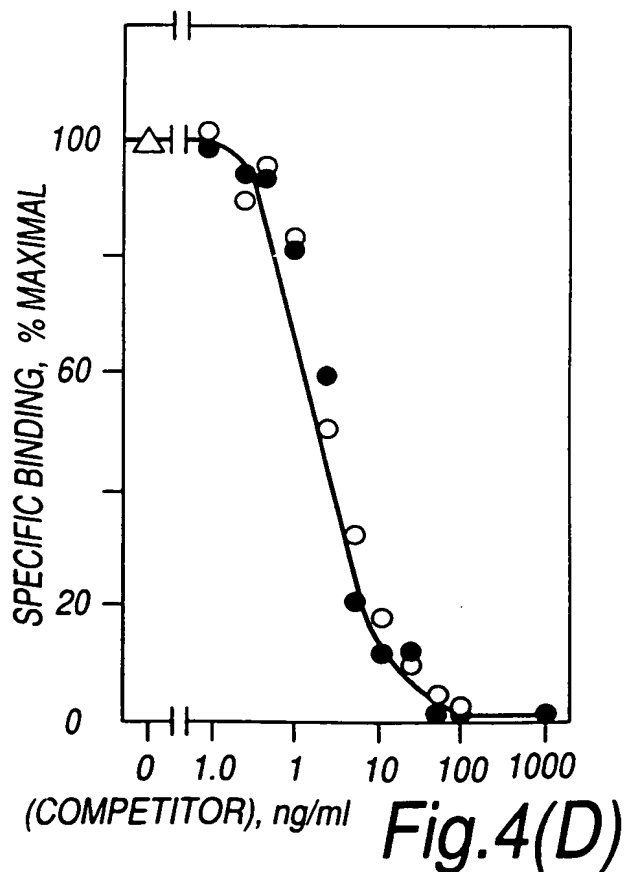
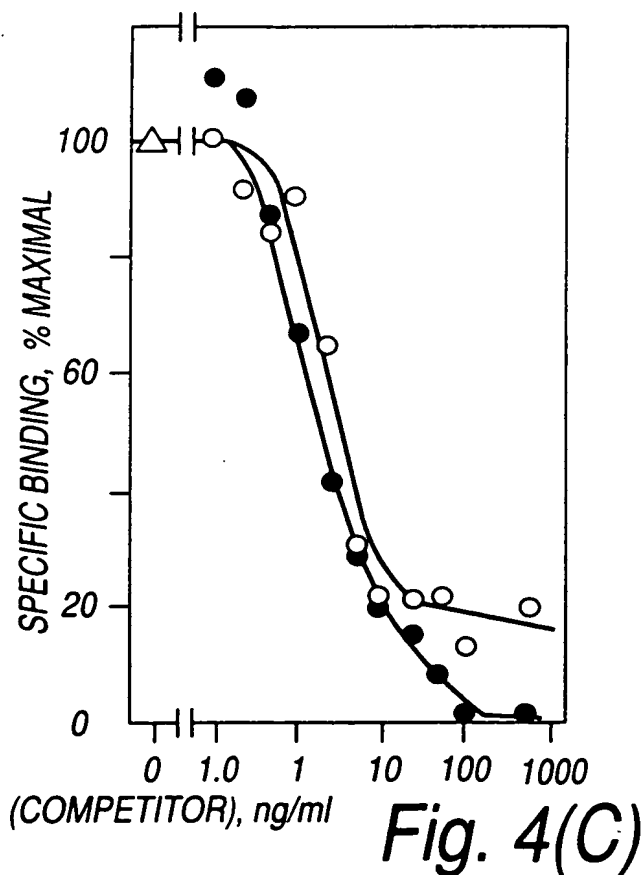
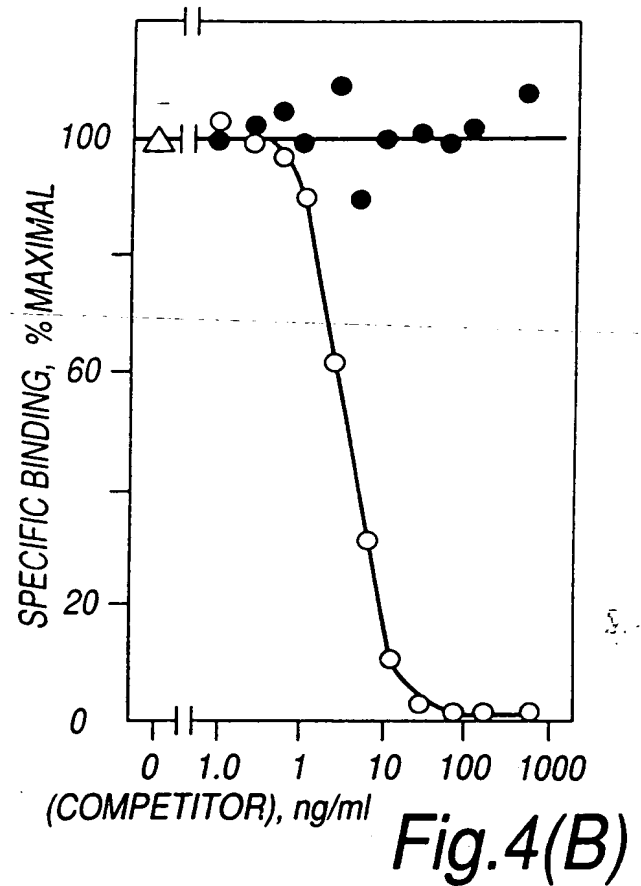
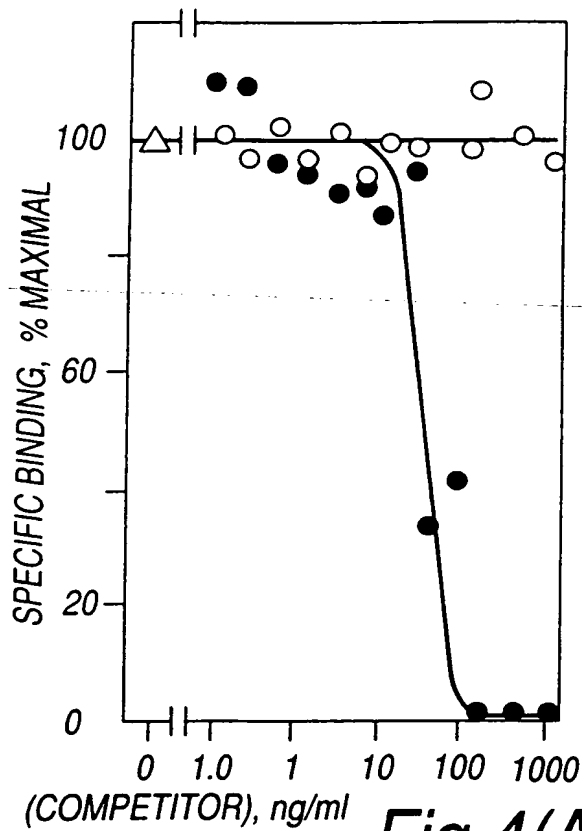


Fig. 3(C)

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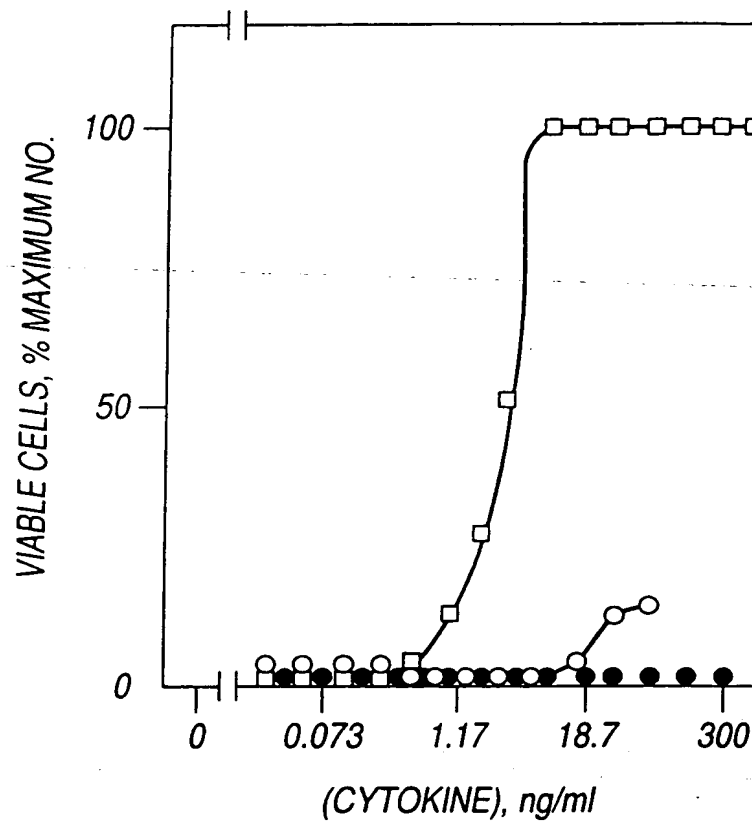


Fig. 5(A)

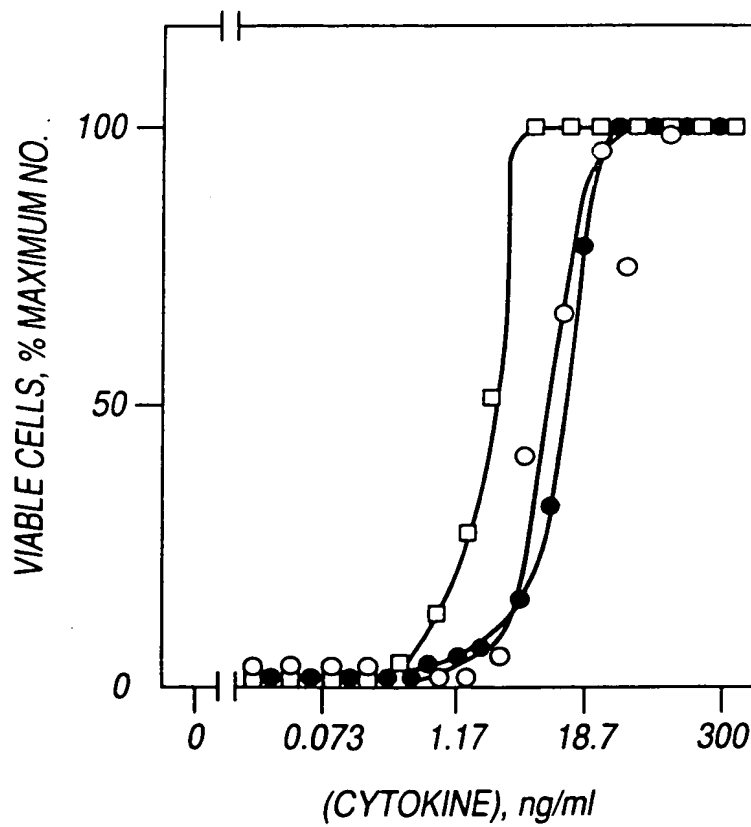


Fig. 5(B)

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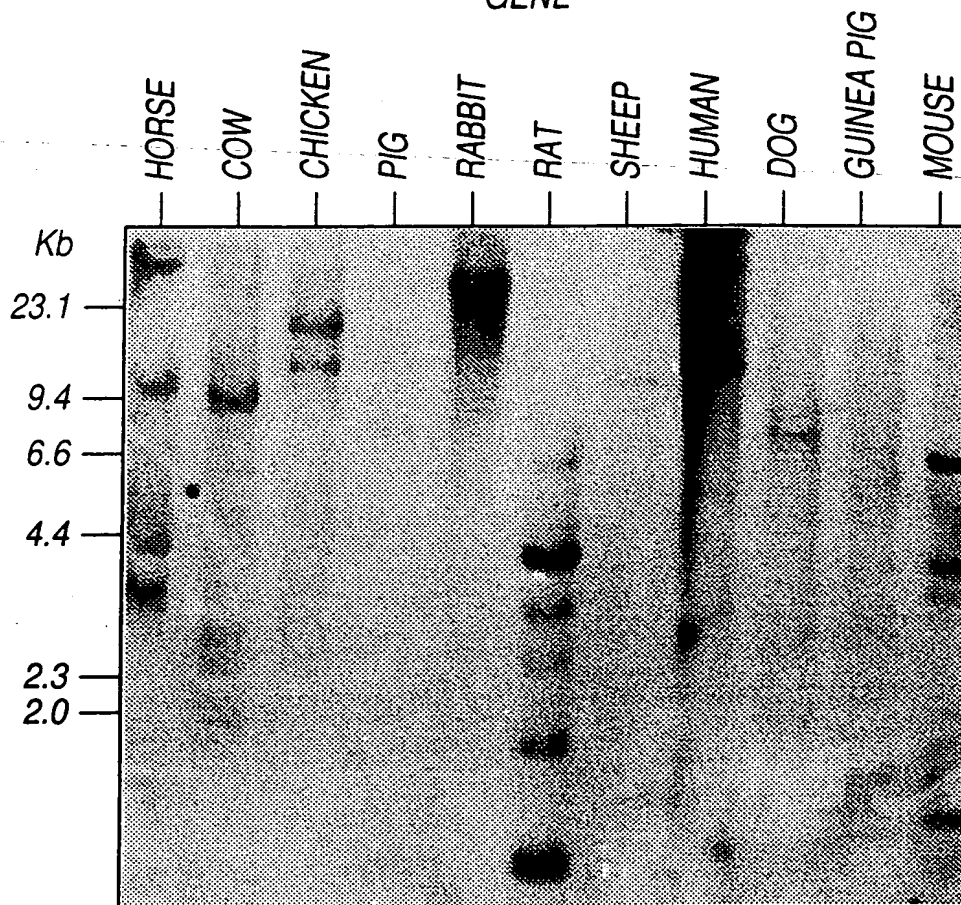
CROSS-SPECIES CONSERVATION OF THE NR-4 (IL-13R α)
GENE

Fig. 6

(major)

DYKDD	DDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

(minor)

ASISS	SDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

Fig. 10

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16/24	17/24
18/24	19/24
20/24	21/24
22/24	23/24

Fig. 7

356290" E48T5060

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09051843-062299B

H gagtctaacacggaccaaggagtttaac

M -60 tgaaaagatagaataaatggcctcgtgc

H M E W P A R L C G
ATGGAGTGGCCGGCGCGGCTCTGCGGGC
* * * *

M 1 ATGGCGCGGCCAGCGCTGCTGGGCGAGC

M 1 M A R P A L L G E

H G G G G A P T E T
H GGGGGCGGGGGGCGCGCCTACGGAACTC
* * * *

M 61 GGCCAAGTTGCCGCGGCCACAGAAGTTC

M 21 G Q V A A A T E V

H E N L C T V I W T
H GAAAACCTCTGCACAGTAATATGGACAT
* * * * * * * *

M 121 GAAAATCTCTGCACGATAATATGGACGT

M 41 E N L C T I I W T

H S L W Y F S H F G
H AGTCTATGGTATTTTAGTCATTTTGGCG
* * * * * *

M 181 ACTCTCAGATATTTTAGTCACTTTGATG

M 61 T L R Y F S H F D

Fig. 7(i)

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acgtgcgggccgggttccgagggcgagaggctgc

.....

cgaattcgggcacgagccgagggcgagggcctgc

L W A L L L C A G G G G
 TGTGGGCGCTGCTGCTCTGCGCCGGCGGGGGGC
 * * * *

TGTTGGTGCTGCTACTGTGGACCGCCACCGTG - - -
 L L V L L L W T A T V -

Q P P V T N L S V S V
 AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
 * * * * * * * * *

AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
 Q P P V T N L S V S V

W N P P E G A S S N C
 GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
 * * * * * * * *

GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
 W S P P E G A S P N C

D K Q D K K I A P E T
 ACAAACAAGATAAGAAAATAGCTCCGGAAACT
 * * * * * * * *

ACCAACAGGATAAGAAAATTGCTCCAGAAACT
 D Q Q D K K I A P E T

Fig. 7(ii)

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H		R	R	S	I	E	V	P	L	N
H		CGTCGTTCAATAGAGTACCCCTGAATG								
		*			*		*	*		
M	241	CATCGTAAAGAGGAATTACCCCTGGATG								
M	81	H	R	K	E	E	L	P	L	D
H		S	T	N	E	S	E	K	P	S
H		AGCACCAATGAGAGTGAGAAGCCTAGCA								
		*		*	*	*	*	*	*	*
M	301	AGTGCCAATGAAAGTGAGAAGCCTAGCC								
M	101	S	A	N	E	S	E	K	P	S
H		G	D	P	E	S	A	V	T	E
H		GGTGATCCTGAGTCTGCTGTGACTGAAC								
		*	*	*	*	*	*	*	*	*
M	361	GGTGATCCTGAGTCCGCTGTGACTGAGC								
M	121	G	D	P	E	S	A	V	T	E
H		K	C	S	W	L	P	G	R	N
H		AAGTGTTCTTGGCTCCCTGGAAGGAATA								
		*	*	*	*	*	*	*	*	*
M	421	AAGTGTTCTTGGCTCCCTGGAAGGAATA								
M	141	K	C	S	W	L	P	G	R	N
H		W	H	R	S	L	E	K	I	H
H		TGGCACAGAAGCCTGGAAAAAATTCATC								

Fig. 7(iii)

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E R I C L Q V G S Q C
 AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
 * * * * *
 AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
 E K I C L Q V G S Q C

 I L V E K C I S P P E
 TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
 * * * * *
 CTTTGGTGAAAAAGTGCATCTCACCCCCCTGAA
 P L V K K C I S P P E

 L Q C I W H N L S Y M
 TTCAATGCATTTGGCACAACCTGAGCTACATG
 * * * * *
 TCAAGTGCATTTGGCATAACCTGAGCTATATG
 L K C I W H N L S Y M

 T S P D T N Y T L Y Y
 CCAGTCCCGACACTAACTATACTCTCTACTAT
 * * * * *
 CAAGCCCTGACACACACTATACTCTGTACTAT
 T S P D T H Y T L Y Y

 Q C E N I F R E G Q Y
 AATGTGAAAACATCTTTAGAGAAGGCCAATAC

Fig. 7(iv)

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M 481 TGGTACAGCAGCCTGGAGAAAAGTCGTC
 M 161 W Y S S L E K S R
 H F G C S F D L T K
 H TTTGGTTGTTTCCTTTGATCTGACCAAAG
 * * * * *
 M 541 ATTGCTTGTTTCCTTTAAATTGACTAAAG
 M 181 I A C S F K L T K
 H Q I M V K D N A G
 H CAAATAATGGTCAAGGATAATGCAGGAA
 * * * * *
 M 601 CAAATAATGGTCAAGGATAATGCTGGGA
 M 201 Q I M V K D N A G
 H T S R V K P D P P
 H ACTTCCCGTGTGAAACCTGATCCTCCAC
 * * * * *
 M 661 ACTTCCTATGTGAAACCTGATCCTCCAC
 M 221 T S Y V K P D P P
 H L Y V Q W E N P Q
 H CTATATGTGCAATGGGAGAATCCACAGA
 * * * * *
 M 721 TTATTAGTGCAGTGGAAGAATCCACAAA
 M 241 L L V Q W K N P Q

Fig. 7(v)

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09051843 062998

```

*   *   *   *   *           *   *   *   *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q   C   E   N   I   Y   R   E   G   Q   H

V   K   D   S   S   F   E   Q   H   S   V
TGAAGGATTCCAGTTTTGAACAACACAGTGTC
*               *   *   *               *
TGGAACCT- - -AGTTTTGAACATCAGAACG TT
V   E   P   -   S   F   E   H   Q   N   V

K   I   K   P   S   F   N   I   V   P   L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
*   *           *   *           *   *           *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K   I   R   P   S   C   K   I   V   S   L

H   I   K   N   L   S   F   H   N   D   D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
*   *   *           *               *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H   I   K   H   L   L   L   K   N   G   A

N   F   I   S   R   C   L   F   Y   E   V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
*   *           *   *   *   *           *   *   *
ATTTTAGAAGCAGATGCTTAACCTTATGAAGTG
N   F   R   S   R   C   L   T   Y   E   V

```

Fig. 7(vi)

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H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*		*	*		
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
		*		*			*	*		
M	841	CAGAATTCCGAATCTGATAGAAACATGG								
M	281	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	901	CTTGCCGACGCTGTCTACACAGTCAGAG								
M	301	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*	*	*	
M	961	GACAACAAACTGTGGAGTGATTGGAGTG								
M	321	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I
H		ACACTCTACATAACCATGTTACTCATTG								

Fig. 7(vii)

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H N V F Y V Q E A K C
 ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
 * * * * *
 ATAATATTTTAGAGGTTGAAGAGGACAAATGC
 H N I L E V E E D K C

 E N T S C F M V P G V
 AGAATACATCTTGTTTCATGGTCCCTGGTGTT
 * * * * *
 AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
 E G T S C F Q L P G V

 I R V K T N K L C Y E
 TAAGAGTCAAAACAAATAAGTTATGCTATGAG
 * * * * *
 TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
 V R V K T N K L C F D

 Q E M S I G K K R N S
 AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
 * * * * *
 AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
 E A Q S I G K E Q N S

 V P V I V A G A I I V
 TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

Fig. 7(viii)

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* * * * *
 M 1021 ACCTTCTACACCACCATGTTACTCACCA
 M 341 T F Y T T M L L T
 H L L L Y L K R L K
 H CTCCTGCTTTACCTAAAAAGGCTCAAGA
 * * * * *
 M 1081 CTCCTT TTTTACCTGAAAAGGCTTAAGA
 M 361 L L F Y L K R L K
 H K I F K E M F G D
 H AAGATTTTAAAGAAATGTTTGGAGACC
 * * * * *
 M 1141 AAGATTTTAAAGAAATGTTTGGAGACC
 M 381 K I F K E M F G D
 H D I Y E K Q T K E
 H GACATCTATGAGAAGCAAACCAAGGAGG
 * * * * *
 M 1201 GACATCTATGAGAAACAATCCAAAGAAG
 M 401 D I Y E K Q S K E
 H K K A S Q *
 H AAGAAAGCCTCTCAGTGAtggagataat
 * * *
 M 1261 AAGAAAGCAGCTCCTTGAtgggggagaag
 M 421 K K A A P *

Fig. 7(ix)

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* * * * *

TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
I P V F V A V A V I I

I I I F P P I P D P G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
* * * * *
TCATTATATTTCCCTCCAATTCCTGATCCTGGC
I I I F P P I P D P G

Q N D D T L H W K K Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
* * * * *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q N D D T L H W K K Y

E T D S V V L I E N L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
* * * * *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E T D S V V L I E N L

ttatTTTTaccttcactgtgaccttgagaaga
tgatttctttcttgccttcaatgtgaccctgt

Fig. 7(x)

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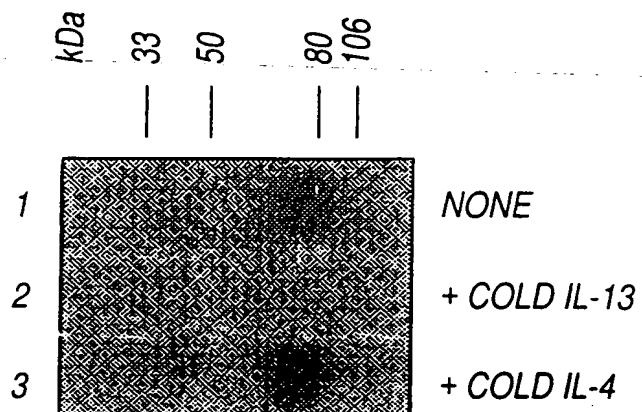


Fig. 8

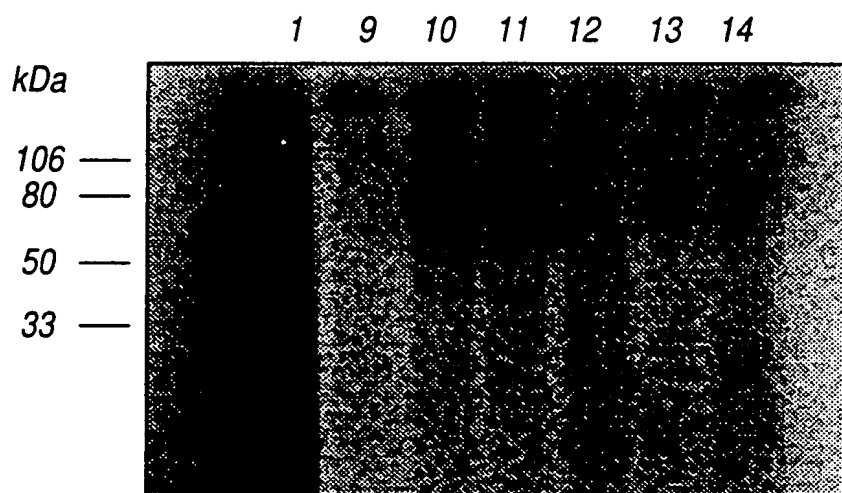


Fig. 9